RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/563,073_
Source: _IFwP_
Date Processed by STIC: _1/13/06_

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IFWP

RAW SEQUENCE LISTING   DATE: 01/13/2006
PATENT APPLICATION: US/10/563,073   TIME: 10:27:40

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\01132006\J563073.raw**

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 3 <110> APPLICANT: DOI, Hirofumi
 4        SAITO, Ken
 6 <120> TITLE OF INVENTION: Method of treating diabetes by inhibiting degradation of at
least one of
 7        CREBL1, ATF6, and HNF-4 alpha by HtrA
 9 <130> FILE REFERENCE: 3190-089
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/563,073
C--> 12 <141> CURRENT FILING DATE: 2005-12-29
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/014377
15 <151> PRIOR FILING DATE: 2004-09-30
17 <150> PRIOR APPLICATION NUMBER: JP P2003-342587
18 <151> PRIOR FILING DATE: 2003-09-30
20 <160> NUMBER OF SEQ ID NOS: 35
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1377
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <223> OTHER INFORMATION: DNA that codes for HtrA2 precursor protein
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37 ggggcattc gctgggggag gagaccccgt ttgacccctg acctccgggc cctgctgacg     120
39 tcaggaactt ctgaccccg ggcccgagtg acttatggga cccccagtct ctgggcccgg     180
41 ttgtctgttg gggtcactga accccgagca tgcctgacgt ctgggacccc gggtccccgg     240
43 gcacaactga ctgcggtgac cccagatacc aggacccggg aggcctcaga gaactctgga     300
45 acccgttcgc gcgcgtggct ggcggtggcg ctgggcgctg ggggggcagt gctgttgttg     360
47 ttgtggggcg ggggtcgggg tcctccggcc gtcctcgccg ccgtccctag cccgccgccc     420
49 gcttctcccc ggagtcagta caacttcatc gcagatgtgg tggagaagac agcacctgcc     480
51 gtggtctata tcgagatcct ggaccggcac cctttcttgg gccgcgaggt ccctatctcg     540
53 aacggctcag gattcgtggt ggctgccgat gggctcattg tcaccaacgc ccatgtggtg     600
55 gctgatcggc gcagagtccg tgtgagactg ctaagcggcg cacgtatga ggccgtggtc     660
57 acagctgtgg atcccgtggc agacatcgca acgctgagga ttcagactaa ggagcctctc     720
59 cccacgctgc tctgggacg ctcagctgat gtccggcaag gggagtttgt tgttgccatg     780
61 ggaagtccct ttgcactgca gaacacgatc acatccggca ttgttagctc tgctcagcgt     840
63 ccagccagag acctgggact ccccaaacc aatgtggaat acattcaaac tgatgcagct     900
65 attgattttg gaaactctgg aggtccctg gttaacctgg atggggaggt gattggagtg     960
67 aacaccatga aggtcacagc tggaatctcc tttgccatc cttctgatcg tcttcgagag    1020
69 tttctgcatc gtggggaaaa gaagaattcc tcctccggaa tcagtgggtc ccagcggcgc    1080
71 tacattgggg tgatgatgct gaccctgagt cccagcatcc ttgctgaact acagcttcga    1140
73 gaaccaagct ttcccgatgt tcagcatggt gtactcatcc ataaagtcat cctgggctcc    1200
75 cctgcacacc gggctggtct gcggcctggt gatgtgattt tggccattgg ggagcagatg    1260
77 gtacaaaatg ctgaagatgt ttatgaagct gttcgaaccc aatcccagtt ggcagtgcag    1320
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83 <211> LENGTH: 458
84 <212> TYPE: PRT
85 <213> ORGANISM: Homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: misc_feature
89 <223> OTHER INFORMATION: HtrA2 precursor protein
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98 Trp Arg Ala Leu Gly Gly Ile Arg Trp Gly Arg Arg Pro Arg Leu Thr
99              20                  25                  30
102 Pro Asp Leu Arg Ala Leu Leu Thr Ser Gly Thr Ser Asp Pro Arg Ala
103         35                  40                  45
106 Arg Val Thr Tyr Gly Thr Pro Ser Leu Trp Ala Arg Leu Ser Val Gly
107     50                  55                  60
110 Val Thr Glu Pro Arg Ala Cys Leu Thr Ser Gly Thr Pro Gly Pro Arg
111 65                  70                  75                  80
114 Ala Gln Leu Thr Ala Val Thr Pro Asp Thr Arg Thr Arg Glu Ala Ser
115             85                  90                  95
118 Glu Asn Ser Gly Thr Arg Ser Arg Ala Trp Leu Ala Val Ala Leu Gly
119             100                 105                 110
122 Ala Gly Gly Ala Val Leu Leu Leu Leu Trp Gly Gly Gly Arg Gly Pro
123             115                 120                 125
126 Pro Ala Val Leu Ala Ala Val Pro Ser Pro Pro Ala Ser Pro Arg
127         130                 135                 140
130 Ser Gln Tyr Asn Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala
131 145                 150                 155                 160
134 Val Val Tyr Ile Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu
135                 165                 170                 175
138 Val Pro Ile Ser Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu
139             180                 185                 190
142 Ile Val Thr Asn Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val
143         195                 200                 205
146 Arg Leu Leu Ser Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp
147     210                 215                 220
150 Pro Val Ala Asp Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu
151 225                 230                 235                 240
154 Pro Thr Leu Pro Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe
155             245                 250                 255
158 Val Val Ala Met Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser
159             260                 265                 270
162 Gly Ile Val Ser Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro
163         275                 280                 285
166 Gln Thr Asn Val Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly
167     290                 295                 300
170 Asn Ser Gly Gly Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val
171 305                 310                 315                 320
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Input Set : **A:\pto.da.txt**
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175             325             330             335
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179             340             345             350
182 Gly Ile Ser Gly Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr
183         355             360             365
186 Leu Ser Pro Ser Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe
187     370             375             380
190 Pro Asp Val Gln His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser
191 385             390             395             400
194 Pro Ala His Arg Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile
195             405             410             415
198 Gly Glu Gln Met Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg
199             420             425             430
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207     450             455
210 <210> SEQ ID NO: 3
211 <211> LENGTH: 981
212 <212> TYPE: DNA
213 <213> ORGANISM: Homo sapiens
215 <220> FEATURE:
216 <221> NAME/KEY: misc_feature
217 <223> OTHER INFORMATION: DNA that codes for mature HtrA2
220 <400> SEQUENCE: 3
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223 gtggtggaga agacagcacc tgccgtggtc tatatcgaga tcctggaccg gcacccttc    120
225 ttgggccgcg aggtccctat ctcgaacggc tcaggattcg tggtggctgc cgatgggctc   180
227 attgtcacca acgcccatgt ggtggctgat cggcgcagag tccgtgtgag actgctaagc   240
229 ggcgacacgt atgaggccgt ggtcacagct gtggatcccg tggcagacat cgcaacgctg   300
231 aggattcaga ctaaggagcc tctccccacg ctgcctctgg acgctcagc tgatgtccgg    360
233 caaggggagt ttgttgttgc catgggaagt ccctttgcac tgcagaacac gatcacatcc   420
235 ggcattgtta gctctgctca gcgtccagcc agagacctgg gactccccca aaccaatgtg   480
237 gaatacattc aaactgatgc agctattgat tttggaaact ctggaggtcc cctggttaac   540
239 ctggatgggg aggtgattgg agtgaacacc atgaaggtca cagctggaat ctcctttgcc   600
241 atcccttctg atcgtcttcg agagtttctg catcgtgggg aaaagaagaa ttcctcctcc   660
243 ggaatcagtg ggtcccagcg cgcgctacat ggggtgatga tgctgacccct gagtcccagc   720
245 atccttgctg aactacagct tcgagaacca agctttcccg atgttcagca tggtgtactc   780
247 atccataaag tcatcctggg ctcccctgca caccgggctg gtctgcggcc tggtgatgtg   840
249 attttggcca ttggggagca gatggtacaa aatgctgaag atgtttatga agctgttcga   900
251 acccaatccc agttggcagt gcagatccgg cggggacgag aaacactgac cttatatgtg   960
253 accctgagg tcacagaatg a                                            981
256 <210> SEQ ID NO: 4
257 <211> LENGTH: 326
258 <212> TYPE: PRT
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
262 <221> NAME/KEY: misc_feature
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263 <223> OTHER INFORMATION: mature HtrA2
266 <400> SEQUENCE: 4
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272 Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile
273   20   25   30
276 Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser
277   35   40   45
280 Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn
281   50   55   60
284 Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val Arg Leu Leu Ser
285 65   70   75   80
288 Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp
289   85   90   95
292 Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro
293   100   105   110
296 Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met
297   115   120   125
300 Gly Ser Pro Phe Ala Leu Gln Asn Thr Ile Thr Ser Gly Ile Val Ser
301   130   135   140
304 Ser Ala Gln Arg Pro Ala Arg Asp Leu Gly Leu Pro Gln Thr Asn Val
305 145   150   155   160
308 Glu Tyr Ile Gln Thr Asp Ala Ala Ile Asp Phe Gly Asn Ser Gly Gly
309   165   170   175
312 Pro Leu Val Asn Leu Asp Gly Glu Val Ile Gly Val Asn Thr Met Lys
313   180   185   190
316 Val Thr Ala Gly Ile Ser Phe Ala Ile Pro Ser Asp Arg Leu Arg Glu
317   195   200   205
320 Phe Leu His Arg Gly Glu Lys Lys Asn Ser Ser Ser Gly Ile Ser Gly
321   210   215   220
324 Ser Gln Arg Arg Tyr Ile Gly Val Met Met Leu Thr Leu Ser Pro Ser
325 225   230   235   240
328 Ile Leu Ala Glu Leu Gln Leu Arg Glu Pro Ser Phe Pro Asp Val Gln
329   245   250   255
332 His Gly Val Leu Ile His Lys Val Ile Leu Gly Ser Pro Ala His Arg
333   260   265   270
336 Ala Gly Leu Arg Pro Gly Asp Val Ile Leu Ala Ile Gly Glu Gln Met
337   275   280   285
340 Val Gln Asn Ala Glu Asp Val Tyr Glu Ala Val Arg Thr Gln Ser Gln
341   290   295   300
344 Leu Ala Val Gln Ile Arg Arg Gly Arg Glu Thr Leu Thr Leu Tyr Val
345 305   310   315   320
348 Thr Pro Glu Val Thr Glu
349   325
352 <210> SEQ ID NO: 5
353 <211> LENGTH: 981
354 <212> TYPE: DNA
355 <213> ORGANISM: Artificial
357 <220> FEATURE:

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   358 <223> OTHER INFORMATION: Polynucleotide consisting of the same base sequence of SEQ
ID NO:
   359       3 wherein the nucleotide of position 520 is g
   361 <220> FEATURE:
   362 <221> NAME/KEY: misc_feature
   363 <223> OTHER INFORMATION: DNA that codes for mature HtrA2(S306A)
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   367 atggccgtcc ctagcccgcc gcccgcttct ccccggagtc agtacaactt catcgcagat    60
   369 gtggtggaga agacagcacc tgccgtggtc tatatcgaga tcctggaccg gcaccctttc   120
   371 ttgggccgcg aggtccctat ctcgaacggc tcaggattcg tggtggctgc cgatgggctc   180
   373 attgtcacca acgcccatgt ggtggctgat cggcgcagag tccgtgtgag actgctaagc   240
   375 ggcgacacgt atgaggccgt ggtcacagct gtggatcccg tggcagacat cgcaacgctg   300
   377 aggattcaga ctaaggagcc tctccccacg ctgcctctgg gacgctcagc tgatgtccgg   360
   379 caaggggagt tgttgttgc catgggaagt ccctttgcac tgcagaacac gatcacatcc   420
   381 ggcattgtta gctctgctca gcgtccagcc agagacctgg gactccccca aaccaatgtg   480
   383 gaatacattc aaactgatgc agctattgat tttggaaacg ctggaggtcc cctggttaac   540
   385 ctggatgggg aggtgattgg agtgaacacc atgaaggtca cagctggaat ctcctttgcc   600
   387 atcccttctg atcgtcttcg agagtttctg catcgtgggg aaaagaagaa ttcctcctcc   660
   389 ggaatcagtg ggtcccagcg cgcgctacatt ggggtgatga tgctgaccct gagtcccagc   720
   391 atccttgctg aactacagct tcgagaacca agctttcccg atgttcagca tggtgtactc   780
   393 atccataaag tcatcctggg ctcccctgca caccgggctg gtctgcggcc tggtgatgtg   840
   395 attttggcca ttggggagca gatggtacaa aatgctgaag atgtttatga agctgttcga   900
   397 acccaatccc agttggcagt gcagatccgg cggggacgag aaacactgac cttatatgtg   960
   399 acccctgagg tcacagaatg a                                             981
   402 <210> SEQ ID NO: 6
   403 <211> LENGTH: 326
   404 <212> TYPE: PRT
   405 <213> ORGANISM: Artificial
   407 <220> FEATURE:
   408 <223> OTHER INFORMATION: Polypeptide consisting of the same amino acid sequence of
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   409       NO:4 wherein the 174th amino acid residue is substituted by Ala
   411 <220> FEATURE:
   412 <221> NAME/KEY: misc_feature
   413 <223> OTHER INFORMATION: mature HtrA2(S306A)
   416 <400> SEQUENCE: 6
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   419 1               5                   10                  15
   422 Phe Ile Ala Asp Val Val Glu Lys Thr Ala Pro Ala Val Val Tyr Ile
   423             20                  25                  30
   426 Glu Ile Leu Asp Arg His Pro Phe Leu Gly Arg Glu Val Pro Ile Ser
   427         35                  40                  45
   430 Asn Gly Ser Gly Phe Val Val Ala Ala Asp Gly Leu Ile Val Thr Asn
   431     50                  55                  60
   434 Ala His Val Val Ala Asp Arg Arg Arg Val Arg Val Arg Leu Leu Ser
   435 65                  70                  75                  80
   438 Gly Asp Thr Tyr Glu Ala Val Val Thr Ala Val Asp Pro Val Ala Asp
   439                 85                  90                  95
   442 Ile Ala Thr Leu Arg Ile Gln Thr Lys Glu Pro Leu Pro Thr Leu Pro
   443             100                 105                 110
   446 Leu Gly Arg Ser Ala Asp Val Arg Gln Gly Glu Phe Val Val Ala Met
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/13/2006
PATENT APPLICATION: **US/10/563,073**   TIME: 10:27:41

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\01132006\J563073.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33

VERIFICATION SUMMARY   DATE: 01/13/2006
PATENT APPLICATION: **US/10/563,073**   TIME: 10:27:41

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\01132006\J563073.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date